

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/536,875  
Source: PCF/10  
Date Processed by STIC: 6/9/05

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 06/09/2005

PATENT APPLICATION: US/10/536,875

TIME: 09:39:42

Input Set : A:\038136-5001-US Sequence Listing.txt

Output Set: N:\CRF4\06092005\J536875.raw

3 <110> APPLICANT: BRIGGS, Kristen  
 4 GLANCY, Todd  
 5 HEIN, Mitch B.  
 6 HIATT, Andrew C.  
 7 KARNOUP, Anton S.  
 8 ANDERSON, W.H. Kerr  
 9 PAREDDY, Dayakar  
 10 PETOLINO, Joseph  
 11 RUBIN-WILSON, Elizabeth  
 12 TAYLOR, Doug  
 13 Roberts, Jean L.  
 14 The Dow Chemical Company  
 15 Dow Agrosiences, LLC  
 16 Epicyte Pharmaceutical, Inc.  
 18 <120> TITLE OF INVENTION: Plant production of immunoglobulins with reduced  
 fucosylation  
 20 <130> FILE REFERENCE: 038136-5001-US  
 C--> 22 <140> CURRENT APPLICATION NUMBER: US/10/536,875  
 C--> 22 <141> CURRENT FILING DATE: 2005-05-27  
 22 <150> PRIOR APPLICATION NUMBER: US 60/429,385  
 23 <151> PRIOR FILING DATE: 2002-11-27  
 25 <150> PRIOR APPLICATION NUMBER: PCT/US03/037905  
 26 <151> PRIOR FILING DATE: 2003-11-28  
 28 <160> NUMBER OF SEQ ID NOS: 85  
 30 <170> SOFTWARE: PatentIn version 3.1  
 32 <210> SEQ ID NO: 1  
 33 <211> LENGTH: 1494  
 34 <212> TYPE: DNA  
 35 <213> ORGANISM: Herpes simplex virus  
 37 <220> FEATURE:  
 38 <221> NAME/KEY: CDS  
 39 <222> LOCATION: (1)..(1494)  
 41 <220> FEATURE:  
 42 <221> NAME/KEY: misc\_feature  
 43 <223> OTHER INFORMATION: HSV Heavy Chain sequence  
 46 <400> SEQUENCE: 1  
 47 atg gga tgg agc tgg atc ttt ctc ttc ctc ctg tca gga gct gca ggt 48  
 48 Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly  
 49 1 5 10 15  
 51 gtc cat tgc cag gtt cag ctc gtg cag tca ggt gct gag gtg aag aag 96  
 52 Val His Cys Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 53 20 25 30  
 55 cct ggc tcc tcg gtg aag gtc tcc tgc aag gct tct gga ggt tcc ttc 144  
 56 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ser Phe

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57	35	40	45	
59	agc tcc tat gct atc aac tgg gtg agg caa gct cct gga caa ggg ctt	192		
60	Ser Ser Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu			
61	50 55 60			
63	gag tgg atg gga ggg ctc atg cct atc ttt ggg aca aca aac tac gcg	240		
64	Glu Trp Met Gly Gly Leu Met Pro Ile Phe Gly Thr Thr Asn Tyr Ala			
65	65 70 75 80			
67	cag aag ttc cag gac agg ctc acg att acc gcg gac gta tcc acg agt	288		
68	Gln Lys Phe Gln Asp Arg Leu Thr Ile Thr Ala Asp Val Ser Thr Ser			
69	85 90 95			
71	aca gcc tac atg caa ctg agc ggc ctg aca tat gaa gac acg gcc atg	336		
72	Thr Ala Tyr Met Gln Leu Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met			
73	100 105 110			
75	tat tac tgt gcg aga gtt gcc tac atg ctt gaa cct acc gtc act gca	384		
76	Tyr Tyr Cys Ala Arg Val Ala Tyr Met Leu Glu Pro Thr Val Thr Ala			
77	115 120 125			
79	ggt ggt ttg gac gtc tgg ggc caa ggg acc ttg gtc acc gtc tcc tcc	432		
80	Gly Gly Leu Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser			
81	130 135 140			
83	gca tcc ccg acc agc ccg aag gtc ttc ccg ctg agc ctc tgt agc acc	480		
84	Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr			
85	145 150 155 160			
87	cag cca gat ggg aac gtg gtc atc gcc tgc ctg gtc cag ggc ttc ttc	528		
88	Gln Pro Asp Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe			
89	165 170 175			
91	cct cag gag cca ctc agt gtg acc tgg agc gaa agc gga cag ggc gtg	576		
92	Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val			
93	180 185 190			
95	acc gcc agg aac ttc cca ccc agc cag gat gcc tcc gga gac ctg tac	624		
96	Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr			
97	195 200 205			
99	acc acg tcc agc cag ctg acc ctt ccg gcc aca cag tgc cta gcg ggc	672		
100	Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly			
101	210 215 220			
103	aag tcc gtg aca tgc cac gtg aag cac tac acg aat ccc agc cag gat	720		
104	Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp			
105	225 230 235 240			
107	gtg act gtg ccc tgc cca gtt ccc tca act cca cct acc cca tct ccc	768		
108	Val Thr Val Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro			
109	245 250 255			
111	tcg act cca cct acc cca tct ccc tca tgc tgc cac ccc agg ctg tca	816		
112	Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser			
113	260 265 270			
115	ctg cac agg cct gcc ctc gag gac ctg ctc tta ggt tcg gaa gcg aac	864		
116	Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn			
117	275 280 285			
119	ctc acg tgc aca ctc acc ggc ctg aga gat gcg tca ggt gtc acc ttc	912		
120	Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe			
121	290 295 300			

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```

123 acc tgg acg ccc tca agt ggt aag agc gct gtt caa ggc cca cct gag      960
124 Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Glu
125 305                      310                      315                      320
127 cgt gac ctg tgt ggc tgc tac agc gtg tcc agt gtc ctt ccg ggc tgt      1008
128 Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys
129                      325                      330                      335
131 gcc gag cct tgg aat cat ggg aag acc ttc act tgc act gct gcc tac      1056
132 Ala Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr
133                      340                      345                      350
135 ccc gag agc aag acc ccg cta acc gcc acc ctg tgc aaa tcc ggc aac      1104
136 Pro Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn
137                      355                      360                      365
139 aca ttc cgg ccc gag gtc cac ctg ctg ccg ccg ccg tgc gag gag ctg      1152
140 Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu
141                      370                      375                      380
143 gcc ctg aac gag ctg gtg acg ctg acg tgc ctg gcg cgc ggc ttc agc      1200
144 Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser
145 385                      390                      395                      400
147 ccc aag gac gtg ctg gtt cgc tgg ctg cag ggc tca cag gag ctg cct      1248
148 Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro
149                      405                      410                      415
151 agg gag aag tac ctg act tgg gca tcc cgg cag gag ccc agc caa ggc      1296
152 Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly
153                      420                      425                      430
155 acc acc acc ttc gct gtg acc tgc ata ctg cgc gtg gca gcc gag gac      1344
156 Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp
157                      435                      440                      445
159 tgg aag aag ggt gac acc ttc tcc tgc atg gtg ggc cac gag gcc ctt      1392
160 Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu
161                      450                      455                      460
163 ccg ctg gcc ttc aca cag aag acc atc gac cgc ttg gcg ggt aaa ccc      1440
164 Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro
165 465                      470                      475                      480
167 acc cat gtc aat gtg tct gtt gtc atg gcg gag gtg gac ggc acc tgc      1488
168 Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Cys
169                      485                      490                      495
171 tac tga      1494
172 Tyr
176 <210> SEQ ID NO: 2
177 <211> LENGTH: 497
178 <212> TYPE: PRT
179 <213> ORGANISM: Herpes simplex virus
181 <400> SEQUENCE: 2
183 Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
184 1                      5                      10                      15
187 Val His Cys Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
188                      20                      25                      30
191 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ser Phe
192                      35                      40                      45

```

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```

195 Ser Ser Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
196      50                      55                      60
199 Glu Trp Met Gly Gly Leu Met Pro Ile Phe Gly Thr Thr Asn Tyr Ala
200 65                      70                      75                      80
203 Gln Lys Phe Gln Asp Arg Leu Thr Ile Thr Ala Asp Val Ser Thr Ser
204                      85                      90                      95
207 Thr Ala Tyr Met Gln Leu Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met
208                      100                      105                      110
211 Tyr Tyr Cys Ala Arg Val Ala Tyr Met Leu Glu Pro Thr Val Thr Ala
212                      115                      120                      125
215 Gly Gly Leu Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
216      130                      135                      140
219 Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr
220 145                      150                      155                      160
223 Gln Pro Asp Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe
224                      165                      170                      175
227 Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val
228                      180                      185                      190
231 Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr
232                      195                      200                      205
235 Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly
236      210                      215                      220
239 Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp
240 225                      230                      235                      240
243 Val Thr Val Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro
244                      245                      250                      255
247 Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser
248                      260                      265                      270
251 Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn
252                      275                      280                      285
255 Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe
256      290                      295                      300
259 Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Glu
260 305                      310                      315                      320
263 Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys
264                      325                      330                      335
267 Ala Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr
268                      340                      345                      350
271 Pro Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn
272                      355                      360                      365
275 Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu
276      370                      375                      380
279 Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser
280 385                      390                      395                      400
283 Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro
284                      405                      410                      415
287 Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly
288                      420                      425                      430
291 Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp

```

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```

292          435          440          445
295 Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu
296          450          455          460
299 Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro
300 465          470          475          480
303 Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Cys
304          485          490          495
307 Tyr
311 <210> SEQ ID NO: 3
312 <211> LENGTH: 57
313 <212> TYPE: DNA
314 <213> ORGANISM: Artificial sequence
316 <220> FEATURE:
317 <223> OTHER INFORMATION: Heavy chain signal peptide
319 <220> FEATURE:
320 <221> NAME/KEY: CDS
321 <222> LOCATION: (1)..(57)
323 <400> SEQUENCE: 3
324 atg gga tgg agc tgg atc ttt ctc ttc ctc ctg tca gga gct gca ggt      48
325 Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
326 1          5          10          15
328 gtc cat tgc      57
329 Val His Cys
333 <210> SEQ ID NO: 4
334 <211> LENGTH: 19
335 <212> TYPE: PRT
336 <213> ORGANISM: Artificial sequence
338 <220> FEATURE:
339 <223> OTHER INFORMATION: Heavy chain signal peptide
341 <400> SEQUENCE: 4
343 Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
344 1          5          10          15
347 Val His Cys
351 <210> SEQ ID NO: 5
352 <211> LENGTH: 1368
353 <212> TYPE: DNA
354 <213> ORGANISM: Artificial sequence
356 <220> FEATURE:
357 <223> OTHER INFORMATION: Mature heavy chain sequence
359 <220> FEATURE:
360 <221> NAME/KEY: CDS
361 <222> LOCATION: (1)..(1368)
363 <400> SEQUENCE: 5
364 cag gtt cag ctc gtg cag tca ggt gct gag gtg aag aag cct ggc tcc      48
365 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
366 1          5          10          15
368 tcg gtg aag gtc tcc tgc aag gct tct gga ggt tcc ttc agc tcc tat      96
369 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ser Phe Ser Ser Tyr
370          20          25          30

```

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/536,875

DATE: 06/09/2005  
TIME: 09:39:43

Input Set : A:\038136-5001-US Sequence Listing.txt  
Output Set: N:\CRF4\06092005\J536875.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:85; N Pos. 9895,9989,10099

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/536,875

DATE: 06/09/2005

TIME: 09:39:43

Input Set : A:\038136-5001-US Sequence Listing.txt

Output Set: N:\CRF4\06092005\J536875.raw

L:22 M:270 C: Current Application Number differs, Replaced Current Application No  
L:22 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:3589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:9840  
M:341 Repeated in SeqNo=85